

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Mathews, Lawrence S.  
Vale, Wylie W.  
Tsuchida, Kunihiro

(ii) TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
(B) STREET: 444 South Flower Street, Suite 2000  
(C) CITY: Los Angeles  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/300,584  
(B) FILING DATE: 02-SEP-1994

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/880,220  
(B) FILING DATE: 08-MAY-1992

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/773,229  
(B) FILING DATE: 09-OCT-1991

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/698,709  
(B) FILING DATE: 10-MAY-1991

(xi) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reiter, Stephen E.  
(B) REGISTRATION NUMBER: 31,192  
(C) REFERENCE/DOCKET NUMBER: P41 9927

(xii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-546-4737  
(B) TELEFAX: 619-546-9392

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2563 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 71..1609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCGAGGAA GACCCAGGGA ACTGGATATC TAGCGAGAAC TTCCCTACGGC TTCTCCGGCG	60
CCTCGGGAAA ATG GGA GCT GCT GCA AAG TTG GCG TTC GCC GTC TTT CTT	109
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu	
1 5 10	
ATC TCT TGC TCT TCA GGT GCT ATA CTT GGC AGA TCA GAA ACT CAG GAG	157
Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu	
15 20 25	
TGT CTT TTC TTT AAT GCT AAT TGG GAA AGA GAC AGA ACC AAC CAG ACT	205
Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr	
30 35 40 45	
GGT GTT GAA CCT TGC TAT GGT GAT AAA GAT AAA CGG CGA CAT TGT TTT	253
Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe	
50 55 60	
GCT ACC TGG AAG AAT ATT TCT GGT TCC ATT GAA ATA GTG AAG CAA GGT	301
Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly	
65 70 75	
TGT TGG CTG GAT ATC AAC TGC TAT GAC AGG ACT GAT TGT ATA GAA	349
Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu	
80 85 90	
AAA AAA GAC AGC CCT GAA GTG TAC TTT TGT TGC TGT GAG GGC AAT ATG	397
Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met	
95 100 105	
TGT AAT GAA AAG TTC TCT TAT TTT CCG GAG ATG GAA GTC ACA CAG CCC	445
Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro	
110 115 120 125	
ACT TCA AAT CCT GTT ACA CCG AAG CCA CCC TAT TAC AAC ATT CTG CTG	493
Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu	
130 135 140	
TAT TCC TTG GTA CCA CTA ATG TTA ATT GCA GGA ATT GTC ATT TGT GCA	541
Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala	
145 150 155	
TTT TGG GTG TAC AGA CAT CAC AAG ATG GCC TAC CCT CCT GTA CTT GTT	589
Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val	
160 165 170	
CCT ACT CAA GAC CCA GGA CCA CCC CCA CCT TCC CCA TTA CTA GGG TTG	637
Pro Thr Gln Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu	
175 180 185	
AAG CCA TTG CAG CTG TTA GAA GTG AAA GCA AGG GGA AGA TTT GGT TGT	685
Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys	
190 195 200 205	
GTC TGG AAA GCC CAG TTG CTC AAT GAA TAT GTG GCT GTC AAA ATA TTT	733
Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe	
210 215 220	

DRAFT - NOT FOR CITATION

CCA ATA CAG GAC AAA CAG TCC TGG CAG AAT GAA TAT GAA GTC TAT AGT Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser 225 230 235	781
CTA CCT GGA ATG AAG CAT GAG AAC ATA CTA CAG TTC ATT GGT GCA GAG Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu 240 245 250	829
AAA AGA GGC ACC AGT GTG GAT GTG GAC CTG TGG CTA ATC ACA GCA TTT Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe 255 260 265	877
CAT GAA AAG GGC TCA CTG TCA GAC TTT CTT AAG GCT AAT GTG GTC TCT His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser 270 275 280 285	925
TGG AAT GAA CTT TGT CAT ATT GCA GAA ACC ATG GCT AGA GGA TTG GCA Trp Asn Glu Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala 290 295 300	973
TAT TTA CAT GAG GAT ATA CCT GGC TTA AAA GAT GGC CAC AAG CCT GCA Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala 305 310 315	1021
ATC TCT CAC AGG GAC ATC AAA AGT AAA AAT GTG CTG TTG AAA AAC AAT Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn 320 325 330	1069
CTG ACA GCT TGC ATT GCT GAC TTT GGG TTG GCC TTA AAG TTC GAG GCT Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala 335 340 345	1117
GCG AAG TCT GCA GGT GAC ACC CAT GGG CAG GTT GGT ACC CCG AGG TAT Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr 350 355 360 365	1165
ATG GCT CCA GAG GTG TTG GAG GGT GCT ATA AAC TTC CAA AGG GAC GCA Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala 370 375 380	1213
TTT CTG AGG ATA GAT ATG TAC GCC ATG GGA TTA GTC CTA TGG GAA TTG Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu 385 390 395	1261
GCT TCT CGT TGC ACT GCT GCA GAT GGA CCC GTA GAT GAG TAC ATG TTA Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu 400 405 410	1309
CCA TTT GAG GAA ATT GGC CAG CAT CCA TCT CTT GAA GAT ATG CAG Pro Phe Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln 415 420 425	1357
GAA GTT GTT GTG CAT AAA AAA AAG AGG CCT GTT TTA AGA GAT TAT TGG Glu Val Val Val His Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp 430 435 440 445	1405
CAG AAA CAT GCA GGA ATG GCA ATG CTC TGT GAA ACG ATA GAA GAA TGT Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys 450 455 460	1453
TGG GAT CAT GAT GCA GAA GCC AGG TTA TCA GCT GGA TGT GTA GGT GAA Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu 465 470 475	1501
AGA ATT ACT CAG ATG CAA AGA CTA ACA AAT ATC ATT ACT ACA GAG GAC Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp 480 485 490	1549

ATT GTA ACA GTG GTC ACA ATG GTG ACA AAT GTT GAC TTT CCT CCC AAA Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys 495 500 505	1597
GAA TCT AGT CTA TGATGGTGGC ACCGTCTGTA CACACTGAGG ACTGGGACTC Glu Ser Ser Leu 510	1649
TGAACGGAG CTGCTAACGCT AAGGAAAGTG CTTAGTTGAT TTTCTGTGTG AAATGAGTAG GATGCCTCCA GGACATGTAC GCAAGCAGCC CCTTGTGGAA AGCATGGATC TGGGAGATGG ATCTGGGAAA CTTACTGCAT CGTCTGCAGC ACAGATATGA AGAGGAGTCT AAGGGAAAAG CTGCAAAC TG TAAAGAAC TT CTGAAAATGT ACTCGAAGAA TGTGCCCTC TCCAAATCAA GGATCTTTG GACCTGGCTA ATCAAGTATT TGCAAAACTG ACATCAGATT TCTTAATGTC TGTCAAGAAGA CACTAATTCC TTAAATGAAC TACTGCTATT TTTTTAAAT GAAAAACTTT TCATTTCAGA TTTTAAAAAG GGTAACTTT TATTGCATTT GCTGTTGTTT CTATAAATGA CTATTGTAAT GCCAACATGA CACAGCTTGT GAATGTGTAG TGTGCTGCTG TTCTGTGTAC ATAGTCATCA AAGTGGGTA CAGTAAAGAG GCTTCCAAGC ATTACTTTAA CCTCCCTCAA CAAGGTATAC CTCAGTTCCA CGGTTGTTAA ATTATAAAAT TGAAAACACT AACAGAATT GAATAAATCA GTCCATGTTT TATAACAAGG TTAATTACAA ATTCACTGTG TTATTTAAGA AAAAATGGTA AGCTATGCTT AGTCCAATA GTAAGTGGCT ATTTGTAAAG CAGTGTGTTA GCTTTCTTC TACTGGCTTG TAATTTAGGG AAAACAAGTG CTGTCTTGA AATGGAAAAG AATATGGTGT CACCCTACCC CCCATACTTA TATCAAGGTC CCAAAATATT CTTTCCATT TCAAAGACAG CACTTGAAA ACCCTAAATT ACAAGCCAGT AGAAGAAAAG CTAAAACACG CTTTACAAAT AGCC	1709 1769 1829 1889 1949 2009 2069 2129 2189 2249 2309 2369 2429 2489 2549 2563

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 513 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys 1 5 10 15
Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe 20 25 30
Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu 35 40 45
Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp 50 55 60
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu 65 70 75 80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu Lys Lys Asp  
85 90 95

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu  
100 105 110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn  
115 120 125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu  
130 135 140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val  
145 150 155 160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln  
165 170 175

Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu  
180 185 190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys  
195 200 205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln  
210 215 220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly  
225 230 235 240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly  
245 250 255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys  
260 265 270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu  
275 280 285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His  
290 295 300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His  
305 310 315 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala  
325 330 335

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser  
340 345 350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
355 360 365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg  
370 375 380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg  
385 390 395 400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu  
405 410 415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val  
420 425 430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His  
435 440 445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His  
450 455 460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr  
465 470 475 480

Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr  
485 490 495

Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser  
500 505 510

Leu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(B) CLONE: XACTR

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 468..1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCCCCACAC AGTGCAGTGA ATAATAGCCG GTGCGGCCCC TCCCCTCTTT CCCTGGCAGT	60
TGTGTATCTG TCACATTGAA GTTGGGCTC CTGTGAGTCT GAGCCTCCCC CTGTGTCTCA	120
TGTGAAGCTG CTGCTGCAGA AGGTGGAGTC GTTGCATGAG GGTGGGGGGA GTGCCTGCTG	180
TTTGATCTGC CTCTGCTCCC CATTACACT CTCATTCAT TCCCACGGAT CCACATTACA	240
ACTCGCCTTT AACCCTTCC CTGGCGGAGC CCACGCGTCT TTCATCCCTC CTGCCCGGCG	300
CGCTGAGCGA CCAGAGCGCG ACATTGTTGC GGCGGGGAT TGGCGACAT TGTTGCGAAT	360
AATCGGAGCT GCTGGGGGG AACTGATACA ACGTTGCGAC TGAAAGGAA TTAACTCGGC	420
CGAATGGGAT TTTATCTGTG TCGGTGAGAG AAGCGGATCC CAGGAGC ATG GGG GCG Met Gly Ala	476
1	
TCT GTA GCG CTG ACT TTT CTA CTT CTT GCA ACT TTC CGC GCA GGC	524
Ser Val Ala Leu Thr Phe Leu Leu Leu Ala Thr Phe Arg Ala Gly	
5 10 15	
TCA GGA CAC GAT GAA GTG GAG ACA AGA GAG TGC ATC TAT TAC AAT GCC	572
Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr Tyr Asn Ala	
20 25 30 35	

DRAFTS 12/2000

AAC TGG GAA CTG GAG AAG ACC AAC CAA AGT GGG GTG GAA AGC TGC GAA Asn Trp Glu Leu Glu Lys Thr Asn Gln Ser Gly Val Glu Ser Cys Glu 40 45 50	620
GGG GAA AAG GAC AAG CGA CTC CAC TGT TAC GCG TCT TGG AGG AAC AAT Gly Glu Lys Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg Asn Asn 55 60 65	668
TCG GGC TTC ATA GAG CTG GTG AAA AAA GGA TGC TGG CTG GAT GAC TTC Ser Gly Phe Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp Asp Phe 70 75 80	716
AAC TGT TAT GAC AGA CAG GAA TGT ATT GCC AAG GAA GAA AAC CCC CAA Asn Cys Tyr Asp Arg Gln Glu Cys Ile Ala Lys Glu Glu Asn Pro Gln 85 90 95	764
GTC TTT TTC TGC TGC GAG GGA AAC TAC TGC AAC AAG AAA TTT ACT Val Phe Phe Cys Cys Glu Gly Asn Tyr Cys Asn Lys Lys Phe Thr 100 105 110 115	812
CAT TTG CCT GAA GTC GAA ACA TTT GAT CCG AAG CCC CAG CCG TCA GCC His Leu Pro Glu Val Glu Thr Phe Asp Pro Lys Pro Gln Pro Ser Ala 120 125 130	860
TCC GTA CTG AAC ATT CTG ATC TAT TCC CTG CTT CCA ATT GTT GGT CTT Ser Val Leu Asn Ile Leu Ile Tyr Ser Leu Leu Pro Ile Val Gly Leu 135 140 145	908
TCC ATG GCA ATT CTC CTG GCG TTC TGG ATG TAC CGT CAT CGA AAG CCT Ser Met Ala Ile Leu Leu Ala Phe Trp Met Tyr Arg His Arg Lys Pro 150 155 160	956
CCC TAC GGG CAT GTA GAG ATC AAT GAG GAC CCC GGT CTG CCC CCT CCA Pro Tyr Gly His Val Glu Ile Asn Glu Asp Pro Gly Leu Pro Pro Pro 165 170 175	1004
TCT CCT CTG GTC GGG CTG AAG CCG CTG CAG TTG CTG GAG ATA AAG GCG Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala 180 185 190 195	1052
CGA GGC CGT TTC GGT GTC GTC TGG AAA GCT CGT CTG CTG AAT GAA TAT Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Arg Leu Leu Asn Glu Tyr 200 205 210	1100
GTC GCA GTG AAA ATC TTC CCC GTG CAG GAT AAG CAG TCG TGG CAG TGT Val Ala Val Lys Ile Phe Pro Val Gln Asp Lys Gln Ser Trp Gln Cys 215 220 225	1148
GAG AAA GAG ATC TTC ACC ACG CCG GGC ATG AAA CAT GAA AAC CTA TTG Glu Lys Glu Ile Phe Thr Thr Pro Gly Met Lys His Glu Asn Leu Leu 230 235 240	1196
GAG TTC ATT GCC GCT GAG AAG AGG GGA AGC AAC CTG GAG ATG GAG CTG Glu Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Met Glu Leu 245 250 255	1244
TGG CTC ATC ACT GCA TTT CAT GAT AAG GGT TCT CTG ACG GAC TAC CTG Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu 260 265 270 275	1292
AAA GGG AAC TTG GTG AGC TGG AAT GAA CTG TGT CAC ATA ACA GAA ACA Lys Gly Asn Leu Val Ser Trp Asn Glu Leu Cys His Ile Thr Glu Thr 280 285 290	1340
ATG GCT CGT GGG CTG GCC TAC TTA CAT GAA GAT GTG CCC CGC TGT AAA Met Ala Arg Gly Leu Ala Tyr Leu His Glu Asp Val Pro Arg Cys Lys 295 300 305	1388

GGT GAA GGG CAC AAA CCT GCA ATC GCT CAC AGA GAT TTT AAA AGT AAG Gly Glu Gly His Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Lys 310 315 320	1436
AAT GTA TTG CTA AGA AAC GAC CTG ACT GCG ATA TTA GCA GAC TTC GGG Asn Val Leu Leu Arg Asn Asp Leu Thr Ala Ile Leu Ala Asp Phe Gly 325 330 335	1484
CTG GCC GTA CGA TTT GAG CCT GGA AAA CCT CCG GGA GAT ACA CAC GGG Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Gly Asp Thr His Gly 340 345 350 355	1532
CAG GTT GGC ACC AGG AGG TAT ATG GCT CCT GAG GTT CTA GAG GGA GCA Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala 360 365 370	1580
ATT AAC TTT CAG CGA GAT TCC TTT CTC AGG ATA GAT ATG TAT GCC ATG Ile Asn Phe Gln Arg Asp Ser Phe Leu Arg Ile Asp Met Tyr Ala Met 375 380 385	1628
GGA CTG GTA CTC TGG GAA ATA GTA TCC CGA TGT ACA GCA GCA GAT GGG Gly Leu Val Leu Trp Glu Ile Val Ser Arg Cys Thr Ala Ala Asp Gly 390 395 400	1676
CCA GTA GAT GAG TAT CTG CTC CCA TTC GAA GAA GAG ATT GGG CAA CAT Pro Val Asp Glu Tyr Leu Leu Pro Phe Glu Glu Ile Gly Gln His 405 410 415	1724
CCT TCC CTA GAG GAT CTG CAA GAA GTT GTC GTT CAC AAG AAG ATA CGC Pro Ser Leu Glu Asp Leu Gln Glu Val Val His Lys Lys Ile Arg 420 425 430 435	1772
CCT GTA TTC AAA GAC CAC TGG CTG AAA CAC CCT GGT CTG GCC CAA CTG Pro Val Phe Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu 440 445 450	1820
TGC GTC ACC ATT GAA GAA TGC TGG GAC CAT GAT GCG GAA GCA CGG CTT Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu 455 460 465	1868
TCG GCA GGC TGC GTA GAG GAG CGT ATT TCC CAA ATC CGT AAA TCA GTG Ser Ala Gly Cys Val Glu Glu Arg Ile Ser Gln Ile Arg Lys Ser Val 470 475 480	1916
AAC GGC ACT ACC TCG GAC TGC CTT GTA TCC ATT GTT ACA TCT GTC ACC Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Ile Val Thr Ser Val Thr 485 490 495	1964
AAT GTG GAC TTG CCG CCC AAA GAG TCC AGT ATC TGAGGTTCT TTGGTCTTTC Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile 500 505 510	2017
CAGACTCACT GACTTTAAA AAAAAAACTC ACGAATGCAG CTGCTATTTT ATCTTGACTT	2077
TTTAATATTT TTTTCTTGG ATTTTACTTG GATCGGATCA ATTTACCAGC ACGTCATTG	2137
AAAGTATTAA AAAAAAAA CAAAACAAA AAGCAAAAC AGACATCTCA GCAAGCATTC	2197
AGGTGCCGAC TTATGAATGC CAATAGGTGC AGGAACCTCA GAACCTAAC AAACCTATT	2257
CTAGAGAATG TTCTCCTGGT TTCCCTTATC TCAGAAGAGG ACCCATAGGA AAACACCTAA	2317
GTCAAGCAAA TGCTGCAG	2335

2006-12-29 14:39:26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 510 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Ser Val Ala Leu Thr Phe Leu Leu Leu Leu Ala Thr Phe  
1 5 10 15

Arg Ala Gly Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr  
20 25 30

Tyr Asn Ala Asn Trp Glu Leu Glu Lys Thr Asn Gln Ser Gly Val Glu  
35 40 45

Ser Cys Glu Gly Glu Lys Asp Lys Arg Leu His Cys Tyr Ala Ser Trp  
50 55 60

Arg Asn Asn Ser Gly Phe Ile Glu Leu Val Lys Lys Gly Cys Trp Leu  
65 70 75 80

Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Ile Ala Lys Glu Glu  
85 90 95

Asn Pro Gln Val Phe Phe Cys Cys Cys Glu Gly Asn Tyr Cys Asn Lys  
100 105 110

Lys Phe Thr His Leu Pro Glu Val Glu Thr Phe Asp Pro Lys Pro Gln  
115 120 125

Pro Ser Ala Ser Val Leu Asn Ile Leu Ile Tyr Ser Leu Leu Pro Ile  
130 135 140

Val Gly Leu Ser Met Ala Ile Leu Leu Ala Phe Trp Met Tyr Arg His  
145 150 155 160

Arg Lys Pro Pro Tyr Gly His Val Glu Ile Asn Glu Asp Pro Gly Leu  
165 170 175

Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu Leu Glu  
180 185 190

Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Arg Leu Leu  
195 200 205

Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Val Gln Asp Lys Gln Ser  
210 215 220

Trp Gln Cys Glu Lys Glu Ile Phe Thr Thr Pro Gly Met Lys His Glu  
225 230 235 240

Asn Leu Leu Glu Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu  
245 250 255

Met Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser Leu Thr  
260 265 270

Asp Tyr Leu Lys Gly Asn Leu Val Ser Trp Asn Glu Leu Cys His Ile  
275 280 285

Thr Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu Asp Val Pro  
290 295 300

DRAFT - 483247/20

Arg Cys Lys Gly Glu Gly His Lys Pro Ala Ile Ala His Arg Asp Phe  
305 310 315 320

Lys Ser Lys Asn Val Leu Leu Arg Asn Asp Leu Thr Ala Ile Leu Ala  
325 330 335

Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp  
340 345 350

Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu  
355 360 365

Glu Gly Ala Ile Asn Phe Gln Arg Asp Ser Phe Leu Arg Ile Asp Met  
370 375 380

Tyr Ala Met Gly Leu Val Leu Trp Glu Ile Val Ser Arg Cys Thr Ala  
385 390 395 400

Ala Asp Gly Pro Val Asp Glu Tyr Leu Leu Pro Phe Glu Glu Ile  
405 410 415

Gly Gln His Pro Ser Leu Glu Asp Leu Gln Glu Val Val Val His Lys  
420 425 430

Lys Ile Arg Pro Val Phe Lys Asp His Trp Leu Lys His Pro Gly Leu  
435 440 445

Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp Ala Glu  
450 455 460

Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Ile Ser Gln Ile Arg  
465 470 475 480

Lys Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Ile Val Thr  
485 490 495

Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile  
500 505 510

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Leu Lys Pro Glu Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /note= "Xaa at position 2 is either "Thr" or "Ser"."

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 5  
(D) OTHER INFORMATION: /note= "Xaa at position 5 is either "Tyr" or "Phe"."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Xaa Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Ile Lys Ser Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Thr Arg Arg Tyr Met  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

DATA REQUESTED  
BY  
SAC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Leu Ala Ala Arg Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is either "Ile" or "Val"."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is either "Lys" or "Arg"."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is either "Thr" or "Met"."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Pro Xaa Xaa Trp Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 72..1553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCCGGGAAC TTCAAAGCGC GCTGCGCGG CGCTCTGGGA CCCCGAAGCC TTGCACCGCC

60

GCGGGGTGGC C ATG ACC CCA GCG CGC CGC TCC GCA CTG AGC CTG GCC CTC  
Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu

1

5

10

110

CTG CTG GTG GCA CTG GCC TCC GAC CTT GCG GCA GGA CTG AAG TGT GTG 158  
Leu Leu Val Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val  
15 20 25

TGT CTT TTG TGT GAT TCC TCA AAC TTT ACC TGC CAA ACC GAA GGA GCA 206  
Cys Leu Leu Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala  
30 35 40 45

TGC TGG GCC TCT GTC ATG CTA ACC AAC GGG AAA GAA CAG GTG AGC AAA 254  
Cys Trp Ala Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys  
50 55 60

TCG TGC GTG TCC CTC CCG GAA CTA AAT GCT CAG GTC TTC TGT CAC AGT 302  
Ser Cys Val Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser  
65 70 75

TCC AAC AAC GTG ACC AAG ACC GAA TGT TGC TTC ACA GAC TTC TGC AAC 350  
Ser Asn Asn Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn  
80 85 90

AAC ATC ACT CAG CAC CTT CCC ACA GCA TCT CCA GAT GCC CCT AGA CTT 398  
Asn Ile Thr Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu  
95 100 105

GGC CCC ACA GAG CTG ACA GTT GTT ATC ACT GTA CCT GTT TGC CTC CTG 446  
Gly Pro Thr Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu  
110 115 120 125

TCC ATC GCA GCC ATG CTA ACG ATA TGG GCC TGC CAG GAC CGC CAG TGC 494  
Ser Ile Ala Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys  
130 135 140

ACA TAC AGG AAG ACC AAG AGA CAC AAT GTG GAG GAA CCA CTG GCA GAG 542  
Thr Tyr Arg Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu  
145 150 155

TAC AGC CTT GTC AAT GCT GGA AAA ACC CTC AAA GAT CTG ATT TAT GAT 590  
Tyr Ser Leu Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp  
160 165 170

GCC ACT GCC TCG GGC TCA GGA TCT GGC CCG CCT CTT TTG GTT CAA AGA 638  
Ala Thr Ala Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg  
175 180 185

ACC ATC GCA AGG ACA ATT GTA CTT CAA GAA ATC GTA GGA AAA GGT CGG 686  
Thr Ile Ala Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg  
190 195 200 205

TTT GGG GAA GTG TGG CAC GGA AGA TGG TGT GGA GAA GAT GTG GCT GTG 734  
Phe Gly Glu Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val  
210 215 220

AAA ATA TTC TCC TCC AGA GAT GAG AGA TCT TGG TTC CGT GAG GCA GAA 782  
Lys Ile Phe Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu  
225 230 235

ATT TAT CAG ACG GTA ATG CTG AGA CAT GAG AAT ATT CTC GGT TTC ATC 830  
Ile Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile  
240 245 250

GCG GCC GAC AAC AAA GAT AAT GGA ACC TGG ACT CAG CTT TGG CTT GTG 878  
Ala Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val  
255 260 265

TCA GAG TAT CAC GAG CAG GGC TCC TTA TAT GAC TAT TTG AAT AGA AAC 270 275 280 285  
Ser Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn

ATA GTG ACC GTG GCT GGA ATG GTC AAG TTG GCG CTT TCA ATA GCG AGT 974  
Ile Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser  
290 295 300

GGT CTG GCT CAC CTA CAC ATG GAG ATC GTG GGC ACT CAA GGT AAG CCT 1022  
Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro  
305 310 315

GCT ATT GCT CAC CGA GAT ATA AAG TCA AAG AAT ATC TTA GTC AAA AAG 1070  
Ala Ile Ala His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys  
320 325 330

TGT GAC ACT TGT GCC ATA GCT GAC TTA GGG CTG GCT GTG AAA CAT GAT 1118  
Cys Asp Thr Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp  
335 340 345

TCT ATC ATG AAC ACT ATA GAT ATA CCC CAG AAT CCT AAA GTG GGA ACC 1166  
Ser Ile Met Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr  
350 355 360 365

AAG AGG TAT ATG GCT CCC GAA ATG CTT GAT GAT ACA ATG AAC GTC AAC 1214  
Lys Arg Tyr Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn  
370 375 380

ATC TTT GAG TCC TTC AAG CGA GCT GAC ATC TAT TCG GTG GGG CTG GTT 1262  
Ile Phe Glu Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val  
385 390 395

TAC TGG GAA ATA GCT CGA AGG TGT TCA GTT GGA GGA CTT GTT GAA GAG 1310  
Tyr Trp Glu Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu  
400 405 410

TAC CAG TTG CCT TAT TAT GAC ATG GTG CCT TCA GAT CCT TCC ATA GAG 1358  
Tyr Gln Leu Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu  
415 420 425

GAA ATG AGG AAG GTC GTT TGT GAT CAG AAA CTG CGA CCA AAT CTC CCA 1406  
Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro  
430 435 440 445

AAC CAG TGG CAA AGC TGT GAG GCG CTC CGG GTC ATG GGA AGA ATA ATG 1454  
Asn Gln Trp Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met  
450 455 460

CGT GAG TGC TGG TAT GCC AAC GGG GCA GCT CGC CTG ACC GCC CTG CGC 1502  
Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg  
465 470 475

GTG AAG AAG ACC ATT TCT CAG CTG TGT GTC AAG GAA GAC TGT AAG GCC 1550  
Val Lys Lys Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
480 485 490

TAAGGATACA GGCGACGGGA AAGCCCTCAC CACTCTCTTT CATGTCTCCT GC 1602

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 493 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu Leu Leu Val  
1 5 10 15

Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val Cys Leu Leu  
20 25 30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala  
35 40 45

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys Ser Cys Val  
50 55 60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn  
65 70 75 80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr  
85 90 95

Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu Gly Pro Thr  
100 105 110

Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala  
115 120 125

Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys Thr Tyr Arg  
130 135 140

Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu Tyr Ser Leu  
145 150 155 160

Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Ala Thr Ala  
165 170 175

Ser Gly Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg Thr Ile Ala  
180 185 190

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu  
195 200 205

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe  
210 215 220

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln  
225 230 235 240

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp  
245 250 255

Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr  
260 265 270

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr  
275 280 285

Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala  
290 295 300

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala  
305 310 315 320  
His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Asp Thr  
325 330 335  
Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Met  
340 345 350  
Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr  
355 360 365  
Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu  
370 375 380  
Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu  
385 390 395 400  
Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu Tyr Gln Leu  
405 410 415  
Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg  
420 425 430  
Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro Asn Gln Trp  
435 440 445  
Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys  
450 455 460  
Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Val Lys Lys  
465 470 475 480  
Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala  
485 490

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
CGGGATCCGT NGCNGTNAAR ATHTTYCC

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
CGGGATCCYT CNGGNGCCAT RTANCKYCTN GTNCC